

Microbial and Molecular Ecology

INL is expanding the classical methods for identifying important microbial communities and for determining their numbers, activities and capabilities. By understanding environmental microbial communities and their physiologies, we can use them for a range of environmental restoration, natural resource recovery and energy-development applications. Molecular biology and surface chemistry disciplines are joined to develop new ecological understanding of single-cell resources in both surface and subsurface environments. With the expansion of microbial genome sequencing, INL research will lead to better understanding and application of microbial processes through detailed knowledge of gene expression under different conditions.

Progress

INL findings indicate the value of both traditional culture-based and molecular nonculture-based methods of characterizing microbial communities. Traditional methods yield isolates from unique environments and allow complete physiological characterization such as that performed on samples from gas hydrate-rich sediments and deep sandstones and shales of hydrocarbon-rich sedimentary deposits. INL molecular ecology methods have led to assays that identify specific microorganisms that prefer to be attached (versus unattached) in the subsurface, diversity

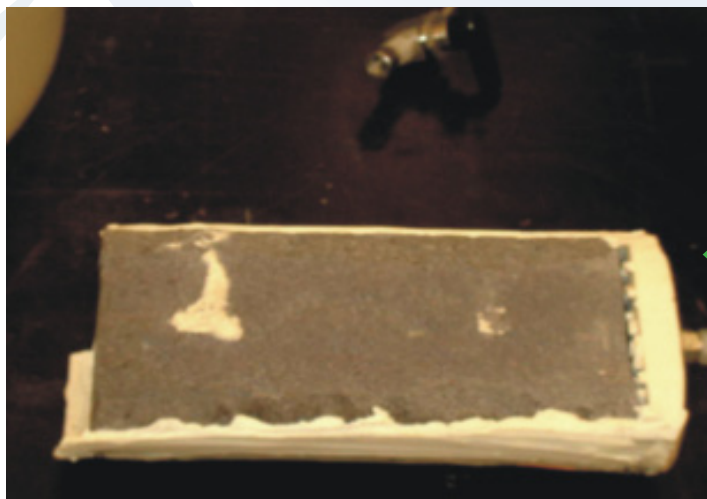
of methanotrophs in a basalt aquifer, aquifer microbes that can increase calcite precipitation, and a heretofore unrecognized archaeal component in an oxic aquifer.

Future goals aim to quantify the volumetric productivity of subsurface microorganisms that are degrading chlorinated hydrocarbons, identify unique messenger ribonucleic acid that signifies bioremedial activities, and directly detect microorganisms on minerals using secondary ion mass spectroscopy.

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Scientists examine deep-sea-floor sediment core containing natural gas hydrate.



This section of a polymer embedded basalt core is used for permeability and microbially mediated porous media transport studies.

The Energy of Innovation

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Selected Publications/Presentations/Patents

D.E. Cummings, S. Spring, and R.F. Rosenzweig, "The Ecology of Iron-Reducing Bacteria in Contaminated and Pristine Environments," In *Manual of Environmental Microbiology*, 2nd edition, Hurst, C. J., R. L. Crawford, G. R. Knudsen, M. J. McInerney, and L. D. Stetzenbach, eds., ASM Press, Washington, DC, 2002.

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R.M. Lehman, F.F. Roberto, D. Early, D.F. Bruhn, S.E. Brink, S.P. O'Connell, M.E. Delwiche and F. Colwell, "Attached and Unattached Microbial Communities in Closely-Paired Groundwater and Core Samples From an Acidic, Crystalline Rock Aquifer," *Appl. Environ. Microbiol.* Vol. 67, 2001, pp. 2095-2106.

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D.E. Cummings, A.W. March, B. Bostick, S. Spring, F. Caccavo, Jr., S. Fendorf, and R.F. Rosenzweig, "Evidence for Microbial Fe(III) Reduction in Anoxic, Mining-Impacted Lake Sediments (Lake Coeur d'Alene, Idaho)," *Appl. Environ. Microbiol.* Vol. 66, 2000, pp.154-162.

T.C. Onstott, T.J. Phelps, F.S. Colwell, D. Ringelberg, D.C. White, D.R. Boone, J.P. McKinley, T.O. Stevens, P.E. Long, D.L. Balkwill, W.T. Griffin, and T. Kieft, "Observations Pertaining to the Origin and Ecology of Microorganisms Recovered from the Deep Subsurface of Taylorsville Basin, Virginia," *Geomicrobiology*, Vol. 15, 1998, pp. 353-385.

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F.S. Colwell, T.C. Onstott, M.E. Delwiche, D. Chandler, J.K. Fredrickson, Q.J. Yao, J.P. McKinley, D.R. Boone, R. Griffiths, T.J. Phelps, D. Ringelberg, D.C. White, L. LaFreniere, D. Balkwill, R.M. Lehman, J. Konisky, and P.E. Long, "Microorganisms from Deep, High Temperature Sandstones: Constraints on Microbial Colonization," *FEMS Microbiology Reviews*, Vol. 20, 1997, pp. 425-435.

For more information

Technical Contacts

Deborah T. Newby, Ph.D.

(208) 526-7779

Deborah.Newby@inl.gov

Yoshiko Fujita, Ph.D.

(208) 526-1242

Yoshiko.Fujita@inl.gov

Management Contact

Don Maiers

(208) 526-6991

Donald.Maiers@inl.gov

www.inl.gov/biologicalsystems

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